

SEQUENCE LISTING

(I) GENERAL INFORMATION:

(i) APPLICANT: University of Pittsburgh of the Commonwealth System  
of Higher Education, 911 William Pitt Union  
Pittsburgh, PA 15260

(ii) TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue  
of a Mammalian Host

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Eckert Seamans Cherin & Mellott, LLC  
(B) STREET: 600 Grant Street, 42nd Floor  
(C) CITY: Pittsburgh  
(D) STATE: PA  
(E) COUNTRY: USA  
(F) ZIP: 15219

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Meyers, Diane R.  
(B) REGISTRATION NUMBER: 38,968  
(C) REFERENCE/DOCKET NUMBER: 109070-11-1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (412) 566-6000  
(B) TELEFAX: (412) 566-6099  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human T-cell cDNA Library
- (B) CLONE: Human Interleukin-1 Receptor

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 55..1764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTCCTGAGA AGCTGGACCC CTTGGTAAAA GACAAGGCCT TCTCCAAGAA GAAT	ATG	57
	Met	
	1	
AAA GTG TTA CTC AGA CTT ATT TGT TTC ATA GCT CTA CTG ATT TCT TCT		105
Lys Val Leu Leu Arg Leu Ile Cys Phe Ile Ala Leu Leu Ile Ser Ser		
	5 10 15	
CTG GAG GCT GAT AAA TGC AAG GAA CGT GAA GAA AAA ATA ATT TTA GTG		153
Leu Glu Ala Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu Val		
	20 25 30	
TCA TCT GCA AAT GAA ATT GAT GTT CGT CCC TGT CCT CTT AAC CCA AAT		201
Ser Ser Ala Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn		
	35 40 45	
GAA CAC AAA GGC ACT ATA ACT TGG TAT AAA GAT GAC AGC AAG ACA CCT		249
Glu His Lys Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro		
	50 55 60 65	
GTA TCT ACA GAA CAA GCC TCC AGG ATT CAT CAA CAC AAA GAG AAA CTT		297
Val Ser Thr Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys Leu		
	70 75 80	
TGG TTT GTT CCT GCT AAG GTG GAG GAT TCA GGA CAT TAC TAT TGC GTG		345
Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val		
	85 90 95	
GTA AGA AAT TCA TCT TAC TGC CTC AGA ATT AAA ATA AGT GCA AAA TTT		393
Val Arg Asn Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe		
	100 105 110	

GTG	GAG	AAT	GAG	CCT	AAC	TTA	TGT	TAT	AAT	GCA	CAA	GCC	ATA	TTT	AAG	441
Val	Glu	Asn	Glu	Pro	Asn	Leu	Cys	Tyr	Asn	Ala	Gln	Ala	Ile	Phe	Lys	
115						120					125					
CAG	AAA	CTA	CCC	GTT	GCA	GGA	GAC	GGA	GGA	CTT	GTG	TGC	CCT	TAT	ATG	489
Gln	Lys	Leu	Pro	Val	Ala	Gly	Asp	Gly	Gly	Leu	Val	Cys	Pro	Tyr	Met	
130					135					140					145	
GAG	TTT	TTT	AAA	AAT	GAA	AAT	AAT	GAG	TTA	CCT	AAA	TTA	CAG	TGG	TAT	537
Glu	Phe	Phe	Lys	Asn	Glu	Asn	Asn	Glu	Leu	Pro	Lys	Leu	Gln	Trp	Tyr	
			150					155						160		
AAG	GAT	TGC	AAA	CCT	CTA	CTT	CTT	GAC	AAT	ATA	CAC	TTT	AGT	GGA	GTC	585
Lys	Asp	Cys	Lys	Pro	Leu	Leu	Leu	Asp	Asn	Ile	His	Phe	Ser	Gly	Val	
			165					170					175			
AAA	GAT	AGG	CTC	ATC	GTG	ATG	AAT	GTG	GCT	GAA	AAG	CAT	AGA	GGG	AAC	633
Lys	Asp	Arg	Leu	Ile	Val	Met	Asn	Val	Ala	Glu	Lys	His	Arg	Gly	Asn	
		180					185					190				
TAT	ACT	TGT	CAT	GCA	TCC	TAC	ACA	TAC	TTG	GGC	AAG	CAA	TAT	CCT	ATT	681
Tyr	Thr	Cys	His	Ala	Ser	Tyr	Thr	Tyr	Leu	Gly	Lys	Gln	Tyr	Pro	Ile	
	195					200					205					
ACC	CGG	GTA	ATA	GAA	TTT	ATT	ACT	CTA	GAG	GAA	AAC	AAA	CCC	ACA	AGG	729
Thr	Arg	Val	Ile	Glu	Phe	Ile	Thr	Leu	Glu	Glu	Asn	Lys	Pro	Thr	Arg	
210					215					220					225	
CCT	GTG	ATT	GTG	AGC	CCA	GCT	AAT	GAG	ACA	ATG	GAA	GTA	GAC	TTG	GGA	777
Pro	Val	Ile	Val	Ser	Pro	Ala	Asn	Glu	Thr	Met	Glu	Val	Asp	Leu	Gly	
				230					235					240		
TCC	CAG	ATA	CAA	TTG	ATC	TGT	AAT	GTC	ACC	GGC	CAG	TTG	AGT	GAC	ATT	825
Ser	Gln	Ile	Gln	Leu	Ile	Cys	Asn	Val	Thr	Gly	Gln	Leu	Ser	Asp	Ile	
			245					250					255			
GCT	TAC	TGG	AAG	TGG	AAT	GGG	TCA	GTA	ATT	GAT	GAA	GAT	GAC	CCA	GTG	873
Ala	Tyr	Trp	Lys	Trp	Asn	Gly	Ser	Val	Ile	Asp	Glu	Asp	Asp	Pro	Val	
		260				265						270				
CTA	GGG	GAA	GAC	TAT	TAC	AGT	GTG	GAA	AAT	CCT	GCA	AAC	AAA	AGA	AGG	921
Leu	Gly	Glu	Asp	Tyr	Tyr	Ser	Val	Glu	Asn	Pro	Ala	Asn	Lys	Arg	Arg	
	275					280					285					
AGT	ACC	CTC	ATC	ACA	GTG	CTT	AAT	ATA	TCG	GAA	ATT	GAA	AGT	AGA	TTT	969
Ser	Thr	Leu	Ile	Thr	Val	Leu	Asn	Ile	Ser	Glu	Ile	Glu	Ser	Arg	Phe	
290					295					300					305	
TAT	AAA	CAT	CCA	TTT	ACC	TGT	TTT	GCC	AAG	AAT	ACA	CAT	GGT	ATA	GAT	1017
Tyr	Lys	His	Pro	Phe	Thr	Cys	Phe	Ala	Lys	Asn	Thr	His	Gly	Ile	Asp	
				310					315					320		
GCA	GCA	TAT	ATC	CAG	TTA	ATA	TAT	CCA	GTC	ACT	AAT	TTC	CAG	AAG	CAC	1065
Ala	Ala	Tyr	Ile	Gln	Leu	Ile	Tyr	Pro	Val	Thr	Asn	Phe	Gln	Lys	His	
			325					330					335			
ATG	ATT	GGT	ATA	TGT	GTC	ACG	TTG	ACA	GTC	ATA	ATT	GTG	TGT	TCT	GTT	1113
Met	Ile	Gly	Ile	Cys	Val	Thr	Leu	Thr	Val	Ile	Ile	Val	Cys	Ser	Val	
		340					345					350				
TTC	ATC	TAT	AAA	ATC	TTC	AAG	ATT	GAC	ATT	GTG	CTT	TGG	TAC	AGG	GAT	1161
Phe	Ile	Tyr	Lys	Ile	Phe	Lys	Ile	Asp	Ile	Val	Leu	Trp	Tyr	Arg	Asp	
	355					360					365					
TCC	TGC	TAT	GAT	TTT	CTC	CCA	ATA	AAA	GCT	TCA	GAT	GGA	AAG	ACC	TAT	1209
Ser	Cys	Tyr	Asp	Phe	Leu	Pro	Ile	Lys	Ala	Ser	Asp	Gly	Lys	Thr	Tyr	
370					375					380					385	

GAC	GCA	TAT	ATA	CTG	TAT	CCA	AAG	ACT	GTT	GGG	GAA	GGG	TCT	ACC	TCT	1257
Asp	Ala	Tyr	Ile	Leu	Tyr	Pro	Lys	Thr	Val	Gly	Glu	Gly	Ser	Thr	Ser	
				390					395					400		
GAC	TGT	GAT	ATT	TTT	GTG	TTT	AAA	GTC	TTG	CCT	GAG	GTC	TTG	GAA	AAA	1305
Asp	Cys	Asp	Ile	Phe	Val	Phe	Lys	Val	Leu	Pro	Glu	Val	Leu	Glu	Lys	
			405					410					415			
CAG	TGT	GGA	TAT	AAG	CTG	TTC	ATT	TAT	GGA	AGG	GAT	GAC	TAC	GTT	GGG	1353
Gln	Cys	Gly	Tyr	Lys	Leu	Phe	Ile	Tyr	Gly	Arg	Asp	Asp	Tyr	Val	Gly	
		420					425					430				
GAA	GAC	ATT	GTT	GAG	GTC	ATT	AAT	GAA	AAC	GTA	AAG	AAA	AGC	AGA	AGA	1401
Glu	Asp	Ile	Val	Glu	Val	Ile	Asn	Glu	Asn	Val	Lys	Lys	Ser	Arg	Arg	
	435					440					445					
CTG	ATT	ATC	ATT	TTA	GTC	AGA	GAA	ACA	TCA	GGC	TTC	AGC	TGG	CTG	GGT	1449
Leu	Ile	Ile	Ile	Leu	Val	Arg	Glu	Thr	Ser	Gly	Phe	Ser	Trp	Leu	Gly	
450					455					460					465	
GGT	TCA	TCT	GAA	GAG	CAA	ATA	GCC	ATG	TAT	AAT	GCT	CTT	GTT	CAG	GAT	1497
Gly	Ser	Ser	Glu	Glu	Gln	Ile	Ala	Met	Tyr	Asn	Ala	Leu	Val	Gln	Asp	
			470						475					480		
GGA	ATT	AAA	GTT	GTC	CTG	CTT	GAG	CTG	GAG	AAA	ATC	CAA	GAC	TAT	GAG	1545
Gly	Ile	Lys	Val	Leu	Leu	Glu	Glu	Leu	Glu	Lys	Ile	Gln	Asp	Tyr	Glu	
		485					490						495			
AAA	ATG	CCA	GAA	TCG	ATT	AAA	TTC	ATT	AAG	CAG	AAA	CAT	GGG	GCT	ATC	1593
Lys	Met	Pro	Glu	Ser	Ile	Lys	Phe	Ile	Lys	Gln	Lys	His	Gly	Ala	Ile	
		500					505					510				
CGC	TGG	TCA	GGG	GAC	TTT	ACA	CAG	GGA	CCA	CAG	TCT	GCA	AAG	ACA	AGG	1641
Arg	Trp	Ser	Gly	Asp	Phe	Thr	Gln	Gly	Pro	Gln	Ser	Ala	Lys	Thr	Arg	
	515					520					525					
TTC	TGG	AAG	AAT	GTC	AGG	TAC	CAC	ATG	CCA	GTC	CAG	CGA	CGG	TCA	CCT	1689
Phe	Trp	Lys	Asn	Val	Arg	Tyr	His	Met	Pro	Val	Gln	Arg	Arg	Ser	Pro	
530				535						540					545	
TCA	TCT	AAA	CAC	CAG	TTA	CTG	TCA	CCA	GCC	ACT	AAG	GAG	AAA	CTG	CAA	1737
Ser	Ser	Lys	His	Gln	Leu	Leu	Ser	Pro	Ala	Thr	Lys	Glu	Lys	Leu	Gln	
			550						555					560		
AGA	GAG	GCT	CAC	GTG	CCT	CTC	GGG	TAGCATGGA								1770
Arg	Glu	Ala	His	Val	Pro	Leu	Gly									
			565				570									

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 569 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Val	Leu	Leu	Arg	Leu	Ile	Cys	Phe	Ile	Ala	Leu	Leu	Ile	Ser
1			5			10					15				

Ser Leu Glu Ala Asp Lys Cys Lys Glu Arg Glu Glu Lys Ile Ile Leu  
20 25 30

Val Ser Ser Ala Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro  
35 40 45

Asn Glu His Lys Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr  
50 55 60

Pro Val Ser Thr Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys  
65 70 75 80

Leu Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys  
85 90 95

Val Val Arg Asn Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys  
100 105 110

Phe Val Glu Asn Glu Pro Asn Leu Cys Tyr Asn Ala Gln Ala Ile Phe  
115 120 125

Lys Gln Lys Leu Pro Val Ala Gly Asp Gly Gly Leu Val Cys Pro Tyr  
130 135 140

Met Glu Phe Phe Lys Asn Glu Asn Asn Glu Leu Pro Lys Leu Gln Trp  
145 150 155 160

Tyr Lys Asp Cys Lys Pro Leu Leu Leu Asp Asn Ile His Phe Ser Gly  
165 170 175

Val Lys Asp Arg Leu Ile Val Met Asn Val Ala Glu Lys His Arg Gly  
180 185 190

Asn Tyr Thr Cys His Ala Ser Tyr Thr Tyr Leu Gly Lys Gln Tyr Pro  
195 200 205

Ile Thr Arg Val Ile Glu Phe Ile Thr Leu Glu Glu Asn Lys Pro Thr  
210 215 220

Arg Pro Val Ile Val Ser Pro Ala Asn Glu Thr Met Glu Val Asp Leu  
225 230 235 240

Gly Ser Gln Ile Gln Leu Ile Cys Asn Val Thr Gly Gln Leu Ser Asp  
245 250 255

Ile Ala Tyr Trp Lys Trp Asn Gly Ser Val Ile Asp Glu Asp Asp Pro  
260 265 270

Val Leu Gly Glu Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg  
275 280 285

Arg Ser Thr Leu Ile Thr Val Leu Asn Ile Ser Glu Ile Glu Ser Arg  
290 295 300

Phe Tyr Lys His Pro Phe Thr Cys Phe Ala Lys Asn Thr His Gly Ile  
305 310 315 320

Asp Ala Ala Tyr Ile Gln Leu Ile Tyr Pro Val Thr Asn Phe Gln Lys  
325 330 335

His Met Ile Gly Ile Cys Val Thr Leu Thr Val Ile Ile Val Cys Ser  
340 345 350

Val Phe Ile Tyr Lys Ile Phe Lys Ile Asp Ile Val Leu Trp Tyr Arg  
355 360 365

Asp Ser Cys Tyr Asp Phe Leu Pro Ile Lys Ala Ser Asp Gly Lys Thr  
370 375 380

Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys Thr Val Gly Glu Gly Ser Thr  
385 390 395 400

Ser Asp Cys Asp Ile Phe Val Phe Lys Val Leu Pro Glu Val Leu Glu  
405 410 415

Lys Gln Cys Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp Asp Tyr Val  
420 425 430

Gly Glu Asp Ile Val Glu Val Ile Asn Glu Asn Val Lys Lys Ser Arg  
435 440 445

Arg Leu Ile Ile Ile Leu Val Arg Glu Thr Ser Gly Phe Ser Trp Leu  
450 455 460

Gly Gly Ser Ser Glu Glu Gln Ile Ala Met Tyr Asn Ala Leu Val Gln  
465 470 475 480

Asp Gly Ile Lys Val Val Leu Leu Glu Leu Glu Lys Ile Gln Asp Tyr  
485 490 495

Glu Lys Met Pro Glu Ser Ile Lys Phe Ile Lys Gln Lys His Gly Ala  
500 505 510

Ile Arg Trp Ser Gly Asp Phe Thr Gln Gly Pro Gln Ser Ala Lys Thr  
515 520 525

Arg Phe Trp Lys Asn Val Arg Tyr His Met Pro Val Gln Arg Arg Ser  
530 535 540

Pro Ser Ser Lys His Gln Leu Leu Ser Pro Ala Thr Lys Glu Lys Leu  
545 550 555 560

Gln Arg Glu Ala His Val Pro Leu Gly  
565

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Mouse T-cell cDNA Library
- (B) CLONE: Mouse Interleukin-1 Receptor

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..1776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATGTCATC AGAGTTCCCA GTGCCCCGAA CCGTGAACAA CACAA ATG GAG AAT	54
Met Glu Asn	
1	
ATG AAA GTG CTA CTG GGG CTC ATT TGT CTC ATG GTG CCT CTG CTG TCG	102
Met Lys Val Leu Leu Gly Leu Ile Cys Leu Met Val Pro Leu Leu Ser	
5 10 15	
CTG GAG ATT GAC GTA TGT ACA GAA TAT CCA AAT CAG ATC GTT TTG TTT	150
Leu Glu Ile Asp Val Cys Thr Glu Tyr Pro Asn Gln Ile Val Leu Phe	
20 25 30 35	
TTA TCT GTA AAT GAA ATT GAT ATT CGC AAG TGT CCT CTT ACT CCA AAT	198
Leu Ser Val Asn Glu Ile Asp Ile Arg Lys Cys Pro Leu Thr Pro Asn	
40 45 50	
AAA ATG CAC GGC GAC ACC ATA ATT TGG TAC AAG AAT GAC AGC AAG ACC	246
Lys Met His Gly Asp Thr Ile Ile Trp Tyr Lys Asn Asp Ser Lys Thr	
55 60 65	
CCC ATA TCA GCG GAC CGG GAC TCC AGG ATT CAT CAG CAG AAT GAA CAT	294
Pro Ile Ser Ala Asp Arg Asp Ser Arg Ile His Gln Gln Asn Glu His	
70 75 80	

CTT	TGG	TTT	GTA	CCT	GCC	AAG	GTG	GAG	GAC	TCA	GGA	TAT	TAC	TAT	TGT	342
Leu	Trp	Phe	Val	Pro	Ala	Lys	Val	Glu	Asp	Ser	Gly	Tyr	Tyr	Tyr	Cys	
	85					90					95					
ATA	GTA	AGA	AAC	TCA	ACT	TAC	TGC	CTC	AAA	ACT	AAA	GTA	ACC	GTA	ACT	390
Ile	Val	Arg	Asn	Ser	Thr	Tyr	Cys	Leu	Lys	Thr	Lys	Val	Thr	Val	Thr	
100					105					110					115	
GTG	TTA	GAG	AAT	GAC	CCT	GGC	TTG	TGT	TAC	AGC	ACA	CAG	GCC	ACC	TTC	438
Val	Leu	Glu	Asn	Asp	Pro	Gly	Leu	Cys	Tyr	Ser	Thr	Gln	Ala	Thr	Phe	
				120					125					130		
CCA	CAG	CGG	CTC	CAC	ATT	GCC	GGG	GAT	GGA	AGT	CTT	GTG	TGC	CCT	TAT	486
Pro	Gln	Arg	Leu	His	Ile	Ala	Gly	Asp	Gly	Ser	Leu	Val	Cys	Pro	Tyr	
			135					140					145			
GTG	AGT	TAT	TTT	AAA	GAT	GAA	AAT	AAT	GAG	TTA	CCC	GAG	GTC	CAG	TGG	534
Val	Ser	Tyr	Phe	Lys	Asp	Glu	Asn	Asn	Glu	Leu	Pro	Glu	Val	Gln	Trp	
		150					155					160				
TAT	AAG	AAC	TGT	AAA	CCT	CTG	CTT	CTT	GAC	AAC	GTG	AGC	TTC	TTC	GGA	582
Tyr	Lys	Asn	Cys	Lys	Pro	Leu	Leu	Leu	Asp	Asn	Val	Ser	Phe	Phe	Gly	
	165					170					175					
GTA	AAA	GAT	AAA	CTG	TTG	GTG	AGG	AAT	GTG	GCT	GAA	GAG	CAC	AGA	GGG	630
Val	Lys	Asp	Lys	Leu	Leu	Val	Arg	Asn	Val	Ala	Glu	Glu	His	Arg	Gly	
180					185					190					195	
GAC	TAT	ATA	TGC	CGT	ATG	TCC	TAT	ACG	TTC	CGG	GGG	AAG	CAA	TAT	CCG	678
Asp	Tyr	Ile	Cys	Arg	Met	Ser	Tyr	Thr	Phe	Arg	Gly	Lys	Gln	Tyr	Pro	
				200					205					210		
GTC	ACA	CGA	GTA	ATA	CAA	TTT	ATC	ACA	ATA	GAT	GAA	AAC	AAG	AGG	GAC	726
Val	Thr	Arg	Val	Ile	Gln	Phe	Ile	Thr	Ile	Asp	Glu	Asn	Lys	Arg	Asp	
			215					220					225			
AGA	CCT	GTT	ATC	CTG	AGC	CCT	CGG	AAT	GAG	ACG	ATC	GAA	GCT	GAC	CCA	774
Arg	Pro	Val	Ile	Leu	Ser	Pro	Arg	Asn	Glu	Thr	Ile	Glu	Ala	Asp	Pro	
		230					235					240				
GGA	TCA	ATG	ATA	CAA	CTG	ATC	TGC	AAC	GTC	ACG	GGC	CAG	TTC	TCA	GAC	822
Gly	Ser	Met	Ile	Gln	Leu	Ile	Cys	Asn	Val	Thr	Gly	Gln	Phe	Ser	Asp	
	245					250					255					
CTT	GTC	TAC	TGG	AAG	TGG	AAT	GGA	TCA	GAA	ATT	GAA	TGG	AAT	GAT	CCA	870
Leu	Val	Tyr	Trp	Lys	Trp	Asn	Gly	Ser	Glu	Ile	Glu	Trp	Asn	Asp	Pro	
260					265					270					275	
TTT	CTA	GCT	GAA	GAC	TAT	CAA	TTT	GTG	GAA	CAT	CCT	TCA	ACC	AAA	AGA	918
Phe	Leu	Ala	Glu	Asp	Tyr	Gln	Phe	Val	Glu	His	Pro	Ser	Thr	Lys	Arg	
				280					285					290		
AAA	TAC	ACA	CTC	ATT	ACA	ACA	CTT	AAC	ATT	TCA	GAA	GTT	AAA	AGC	CAG	966
Lys	Tyr	Thr	Leu	Ile	Thr	Thr	Leu	Asn	Ile	Ser	Glu	Val	Lys	Ser	Gln	
			295					300					305			
TTT	TAT	CGC	TAT	CCG	TTT	ATC	TGT	GTT	GTT	AAG	AAC	ACA	AAT	ATT	TTT	1014
Phe	Tyr	Arg	Tyr	Pro	Phe	Ile	Cys	Val	Val	Lys	Asn	Thr	Asn	Ile	Phe	
		310					315					320				
GAC	TCG	GCG	CAT	GTG	CAG	TTA	ATA	TAC	CCA	GTC	CCT	GAC	TTC	AAG	AAT	1062
Glu	Ser	Ala	His	Val	Gln	Leu	Ile	Tyr	Pro	Val	Pro	Asp	Phe	Lys	Asn	
	325					330					335					
TAC	CTC	ATC	GGG	GGC	TTT	ATC	ATC	CTC	ACG	GCT	ACA	ATT	GTA	TGC	TGT	1110
Tyr	Leu	Ile	Gly	Gly	Phe	Ile	Ile	Leu	Thr	Ala	Thr	Ile	Val	Cys	Cys	
340					345					350					355	



GTG	TGC	ATC	TAT	AAA	GTC	TTC	AAG	GTT	GAC	ATA	GTG	CTT	TGG	TAC	AGG	1158
Val	Cys	Ile	Tyr	Lys	Val	Phe	Lys	Val	Asp	Ile	Val	Leu	Trp	Tyr	Arg	
				360					365						370	
GAC	TCC	TGC	TCT	GGT	TTT	CTT	CCT	TCA	AAA	GCT	TCA	GAT	GGA	AAG	ACA	1206
Asp	Ser	Cys	Ser	Gly	Phe	Leu	Pro	Ser	Lys	Ala	Ser	Asp	Gly	Lys	Thr	
			375					380					385			
TAC	GAT	GCA	TAT	ATT	CTT	TAT	CCC	AAG	ACC	CTG	GGA	GAG	GGG	TCC	TTC	1254
Tyr	Asp	Ala	Tyr	Ile	Leu	Tyr	Pro	Lys	Thr	Leu	Gly	Glu	Gly	Ser	Phe	
		390					395					400				
TCA	GAC	TTA	GAT	ACT	TTT	GTT	TTT	AAA	CTG	TTG	CCT	GAG	GTC	TTG	GAG	1302
Ser	Asp	Leu	Asp	Thr	Phe	Val	Phe	Lys	Leu	Leu	Pro	Glu	Val	Leu	Glu	
	405					410					415					
GGA	CAG	TTT	GGA	TAC	AAG	CTG	TTC	ATT	TAT	GGA	AGG	GAT	GAC	TAT	GTT	1350
Gly	Gln	Phe	Gly	Tyr	Lys	Leu	Phe	Ile	Tyr	Gly	Arg	Asp	Asp	Tyr	Val	
	420				425					430					435	
GGA	GAA	GAT	ACC	ATC	GAG	GTT	ACT	AAT	GAA	AAT	GTA	AAG	AAA	AGC	AGG	1398
Gly	Glu	Asp	Thr	Ile	Glu	Val	Thr	Asn	Glu	Asn	Val	Lys	Lys	Ser	Arg	
				440					445					450		
AGG	CTG	ATT	ATC	ATT	CTA	GTG	AGA	GAT	ATG	GGA	GGC	TTC	AGC	TGG	CTG	1446
Arg	Leu	Ile	Ile	Ile	Leu	Val	Arg	Asp	Met	Gly	Gly	Phe	Ser	Trp	Leu	
			455					460					465			
GGC	CAG	TCA	TCT	GAA	GAG	CAA	ATA	GCC	ATA	TAC	AAT	GCT	CTC	ATC	CAG	1494
Gly	Gln	Ser	Ser	Glu	Glu	Gln	Ile	Ala	Ile	Tyr	Asn	Ala	Leu	Ile	Gln	
		470					475					480				
GAA	GGA	ATT	AAA	ATC	GTC	CTG	CTT	GAG	TTG	GAG	AAA	ATC	CAA	GAC	TAT	1542
Glu	Gly	Ile	Lys	Ile	Val	Leu	Leu	Glu	Leu	Glu	Lys	Ile	Gln	Asp	Tyr	
	485					490					495					
GAG	AAA	ATG	CCA	GAT	TCT	ATT	CAG	TTC	ATT	AAG	CAG	AAA	CAC	GGA	GTC	1590
Glu	Lys	Met	Pro	Asp	Ser	Ile	Gln	Phe	Ile	Lys	Gln	Lys	His	Gly	Val	
	500				505					510					515	
ATT	TGC	TGG	TCA	GGA	GAC	TTT	CAA	GAA	AGA	CCA	CAG	TCT	GCA	AAG	ACC	1638
Ile	Cys	Trp	Ser	Gly	Asp	Phe	Gln	Glu	Arg	Pro	Gln	Ser	Ala	Lys	Thr	
				520					525					530		
AGG	TTC	TGG	AAA	AAC	TTA	AGA	TAC	CAG	ATG	CCA	GCC	CAA	CGG	AGA	TCA	1686
Arg	Phe	Trp	Lys	Asn	Leu	Arg	Tyr	Gln	Met	Pro	Ala	Gln	Arg	Arg	Ser	
			535					540					545			
CCA	TTG	TCT	AAA	CAC	CGC	TTA	CTA	ACC	CTG	GAT	CCT	GTG	CGG	GAC	ACT	1734
Pro	Leu	Ser	Lys	His	Arg	Leu	Leu	Thr	Leu	Asp	Pro	Val	Arg	Asp	Thr	
		550					555					560				
AAG	GAG	AAA	CTG	CCG	GCA	GCA	ACA	CAC	TTA	CCA	CTC	GGC	TAG	CAT	GGC	1782
Lys	Glu	Lys	Leu	Pro	Ala	Ala	Thr	His	Leu	Pro	Leu	Gly				
	565					570					575					

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Asn Met Lys Val Leu Leu Gly Leu Ile Cys Leu Met Val Pro  
1 5 10 15

Leu Leu Ser Leu Glu Ile Asp Val Cys Thr Glu Tyr Pro Asn Gln Ile  
20 25 30

Val Leu Phe Leu Ser Val Asn Glu Ile Asp Ile Arg Lys Cys Pro Leu  
35 40 45

Thr Pro Asn Lys Met His Gly Asp Thr Ile Ile Trp Tyr Lys Asn Asp  
50 55 60

Ser Lys Thr Pro Ile Ser Ala Asp Arg Asp Ser Arg Ile His Gln Gln  
65 70 75 80

Asn Glu His Leu Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly Tyr  
85 90 95

Tyr Tyr Cys Ile Val Arg Asn Ser Thr Tyr Cys Leu Lys Thr Lys Val  
100 105 110

Thr Val Thr Val Leu Glu Asn Asp Pro Gly Leu Cys Tyr Ser Thr Gln  
115 120 125

Ala Thr Phe Pro Gln Arg Leu His Ile Ala Gly Asp Gly Ser Leu Val  
130 135 140

Cys Pro Tyr Val Ser Tyr Phe Lys Asp Glu Asn Asn Glu Leu Pro Glu  
145 150 155 160

Val Gln Trp Tyr Lys Asn Cys Lys Pro Leu Leu Leu Asp Asn Val Ser  
165 170 175

Phe Phe Gly Val Lys Asp Lys Leu Leu Val Arg Asn Val Ala Glu Glu  
180 185 190

His Arg Gly Asp Tyr Ile Cys Arg Met Ser Tyr Thr Phe Arg Gly Lys  
195 200 205

Gln Tyr Pro Val Thr Arg Val Ile Gln Phe Ile Thr Ile Asp Glu Asn  
210 215 220

Lys Arg Asp Arg Pro Val Ile Leu Ser Pro Arg Asn Glu Thr Ile Glu  
225 230 235 240

Ala Asp Pro Gly Ser Met Ile Gln Leu Ile Cys Asn Val Thr Gly Gln  
245 250 255

Phe Ser Asp Leu Val Tyr Trp Lys Trp Asn Gly Ser Glu Ile Glu Trp  
260 265 270

Asn Asp Pro Phe Leu Ala Glu Asp Tyr Gln Phe Val Glu His Pro Ser  
275 280 285

Thr Lys Arg Lys Tyr Thr Leu Ile Thr Thr Leu Asn Ile Ser Glu Val  
290 295 300

Lys Ser Gln Phe Tyr Arg Tyr Pro Phe Ile Cys Val Val Lys Asn Thr  
305 310 315 320

Asn Ile Phe Glu Ser Ala His Val Gln Leu Ile Tyr Pro Val Pro Asp  
325 330 335

Phe Lys Asn Tyr Leu Ile Gly Gly Phe Ile Ile Leu Thr Ala Thr Ile  
340 345 350

Val Cys Cys Val Cys Ile Tyr Lys Val Phe Lys Val Asp Ile Val Leu  
355 360 365

Trp Tyr Arg Asp Ser Cys Ser Gly Phe Leu Pro Ser Lys Ala Ser Asp  
370 375 380

Gly Lys Thr Tyr Asp Ala Tyr Ile Leu Tyr Pro Lys Thr Leu Gly Glu  
385 390 395 400

Gly Ser Phe Ser Asp Leu Asp Thr Phe Val Phe Lys Leu Leu Pro Glu  
405 410 415

Val Leu Glu Gly Gln Phe Gly Tyr Lys Leu Phe Ile Tyr Gly Arg Asp  
420 425 430

Asp Tyr Val Gly Glu Asp Thr Ile Glu Val Thr Asn Glu Asn Val Lys  
435 440 445

Lys Ser Arg Arg Leu Ile Ile Ile Leu Val Arg Asp Met Gly Gly Phe  
450 455 460

Ser Trp Leu Gly Gln Ser Ser Glu Glu Gln Ile Ala Ile Tyr Asn Ala  
465 470 475 480

Leu Ile Gln Glu Gly Ile Lys Ile Val Leu Leu Glu Leu Glu Lys Ile  
485 490 495

Gln Asp Tyr Glu Lys Met Pro Asp Ser Ile Gln Phe Ile Lys Gln Lys  
500 505 510

His Gly Val Ile Cys Trp Ser Gly Asp Phe Gln Glu Arg Pro Gln Ser  
515 520 525

Ala Lys Thr Arg Phe Trp Lys Asn Leu Arg Tyr Gln Met Pro Ala Gln  
530 535 540

Arg Arg Ser Pro Leu Ser Lys His Arg Leu Leu Thr Leu Asp Pro Val  
545 550 555 560

Arg Asp Thr Lys Glu Lys Leu Pro Ala Ala Thr His Leu Pro Leu Gly  
565 570 575

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Primer Oligonucleotide to 5' Leader Sequence of  
IL-1 Receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGATCCCC TCCTGAGAAG CT

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Primer Oligonucleotide Upstream of  
Transmembrane Portion of

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGATCCCA TGTGCTACTG G

21

[illegible]